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RAW SEQUENCE LISTING

DATE: 05/01/2002

PATENT APPLICATION: US/10/023,839

TIME: 11:59:46

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Output Set: N:\CRF3\05012002\J023839.raw

1 <110> APPLICANT: DEROSE, Richard
 2 CHAUBET, Nicole
 3 GIGOT, Claude (deceased)
 4 <120> TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
 5 ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
 6 TRANSFORMATION OF PLANTS
 7 <130> FILE REFERENCE: 022650-453
 8 <140> CURRENT APPLICATION NUMBER: 10/023,839
 9 <141> CURRENT FILING DATE: 2001-12-21
 10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/000,062
 W--> 12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29
 14 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 95/08980
 W--> 15 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1995-07-19
 16 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: PatentIn Ver. 2.0
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 20 <211> LENGTH: 1713
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Zea mays
 23 <400> SEQUENCE: 1
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 26 ccatcaagga gatctggggc agcgtcaagc tgccgggggc caagtcgctt tccaaccgga 180
 27 tcctcctact cgccgccctg tccgagggga caacagtggg tgataacctg ctgaacagtg 240
 28 aggatgtcca ctacatgctc ggggccttga ggactcttgg tctctctgtc gaagcggaca 300
 29 aaggtcccaa aagagctgta cttgttggtc ctggtggaaa gttcccagtt gaggatgcta 360
 30 aagaggaagt gcagctcttc ttggggaatg ctggaactgc aatgcggcca ttgacagcag 420
 31 ctgttactgc tgctggtgga aatgcaactt acgtgcttga tggagtacca agaatagagg 480
 32 agagacccat tggcgacttg gttgtcggat tgaagcagct tgggtgcagat gttgattggt 540
 33 tccttgccac tgactgccc cgtgttcgtg tcaatggaat cggagggcta cctggtggca 600
 34 aggtcaagct gtctggctcc atcagcagtc agtacttgag tgcttctgtg atggctgctc 660
 35 ctttggtctt tggggatgtg gagattgaaa tcattgataa attaattctc attccgtacg 720
 36 tcgaaatgac attgagattg atggaccgtt ttggtgtgaa agcagagcat tctgatagct 780
 37 gggacagatt ctacattaag ggaggtcaaa aatacaagtc ccctaaaaat gcctatgttg 840
 38 aaggtgatgc ctcaagcgca agctatttct tggctggtgc tgcaattact ggagggactg 900
 39 tgactgtgga aggttggtgc accaccagtt tgcaggtgga tgtgaagttt gctgaggtac 960
 40 tggagatgat gggagcgaag gttacatgga ccgagactag cgtaactgtt actccccac 1020
 41 cgcgggagcc atttgggagg aaacacctca aggcgattga tgtcaacatc aacaagatgc 1080
 42 ctgatgtcgc catgactctt gctgtggttg ccctctttgc cgatggcccg acagccatca 1140
 43 gagacgtggc ttcttgagga gttaaaggaga ccgagaggat ggttgcgatc cggacggagc 1200
 44 taaccaagct gggagcatct gttgaggaag ggccggacta ctgcatcatc acgccgccg 1260
 45 agaagctgaa cgtgacggcg atcgacacgt acgacgacca caggatggcc atggccttct 1320
 46 cccttgccgc ctgtgccgag gtccccgtca ccatccggga ccctgggtgc acccggaaga 1380

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49 ctgtttttct ctttcacggg attaatgttt gagtctgtaa cgtagttgt ttgtagcaag 1560
50 tttctatttc ggatcttaag tttgtgcact gtaagccaaa tttcatttca agagtgggtc 1620
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55 <211> LENGTH: 1340
56 <212> TYPE: DNA
57 <213> ORGANISM: Zea mays
58 <220> FEATURE:
59 <221> NAME/KEY: CDS
60 <222> LOCATION: (6)..(1337)
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65 ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc 98
66 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
67 20 25 30
68 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
69 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
70 35 40 45
71 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
72 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
73 50 55 60
74 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242
75 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
76 65 70 75
77 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290
78 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
79 80 85 90 95
80 ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt 338
81 Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val
82 100 105 110
83 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga 386
84 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
85 115 120 125
86 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt 434
87 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
88 130 135 140
89 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 482
90 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
91 145 150 155
92 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc 530
93 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
94 160 165 170 175
95 tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg 578
96 Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu

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97		180		185		190	
98	gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att						626
99	Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile						
100		195		200		205	
101	ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa						674
102	Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys						
103		210		215		220	
104	gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa						722
105	Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln						
106		225		230		235	
107	aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc						770
108	Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser						
109		240		245		250	255
110	gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act						818
111	Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr						
112		260		265		270	
113	gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct						866
114	Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala						
115		275		280		285	
116	gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act agc						914
117	Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser						
118		290		295		300	
119	gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc						962
120	Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu						
121		305		310		315	
122	aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act						1010
123	Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr						
124		320		325		330	335
125	ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac						1058
126	Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp						
127		340		345		350	
128	gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg						1106
129	Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg						
130		355		360		365	
131	acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac						1154
132	Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr						
133		370		375		380	
134	tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg						1202
135	Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr						
136		385		390		395	
137	tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc tgt gcc						1250
138	Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala						
139		400		405		410	415
140	gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc						1298
141	Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe						
142		420		425		430	
143	ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa						1340
144	Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn						
145		435		440			

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148 <211> LENGTH: 444
149 <212> TYPE: PRT
150 <213> ORGANISM: Zea mays
151 <400> SEQUENCE: 3
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155             20             25             30
156   Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
157             35             40             45
158   Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
159             50             55             60
160   Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
161             65             70             75             80
162   Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
163             85             90             95
164   Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
165             100            105            110
166   Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
167             115            120            125
168   Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
169             130            135            140
170   Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
171             145            150            155            160
172   Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
173             165            170            175
174   Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
175             180            185            190
176   Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
177             195            200            205
178   Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
179             210            215            220
180   Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
181             225            230            235            240
182   Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
183             245            250            255
184   Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
185             260            265            270
186   Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
187             275            280            285
188   Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
189             290            295            300
190   Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
191             305            310            315            320
192   Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
193             325            330            335
194   Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
195             340            345            350

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196   Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
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198   Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
199           370                      375                      380
200   Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
201           385                      390                      395                      400
202   Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
203           405                      410                      415
204   Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
205           420                      425                      430
206   Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
207           435                      440
209 <210> SEQ ID NO: 4
210 <211> LENGTH: 1340
211 <212> TYPE: DNA
212 <213> ORGANISM: Zea mays
213 <220> FEATURE:
214 <221> NAME/KEY: CDS
215 <222> LOCATION: (6)..(1337)
216 <400> SEQUENCE: 4
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219           1                      5                      10                      15
220   ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc 98
221   Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
222           20                      25                      30
223   cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
224   Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
225           35                      40                      45
226   aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
227   Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
228           50                      55                      60
229   ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242
230   Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
231           65                      70                      75
232   tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290
233   Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
234           80                      85                      90                      95
235   ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt 338
236   Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val
237           100                      105                      110
238   act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga 386
239   Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
240           115                      120                      125
241   atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt 434
242   Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
243           130                      135                      140
244   ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 482
245   Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\05012002\J023839.raw

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